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SEQUENCE LISTING

<110> ADLER, JON ELLIOT TANG, HUIXIAN PRONIN, ALEXEY <120> IDENTIFICATION OF A NOVEL BITTER TASTE RECEPTOR, T2R76 <130> 100337.54260US

<140> 10/628,464 <141> 2003-07-29

<160> 2

<170> PatentIn Ver. 3.2

<210> 1 <211> 957

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(954)

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Ala Ile Ile Leu Val Thr Ile Leu Leu Leu Leu Arg Leu Val Ala Ile
20 25 30

gca ggc aat ggc ttc atc act gct gct ctg ggc gtg gag tgg gtg cta 144
Ala Gly Asn Gly Phe Ile Thr Ala Ala Leu Gly Val Glu Trp Val Leu
35 40 45

cgg aga atg ttg ttg cct tgt gat aag tta ttg gtt agc cta ggg gcc 192 Arg Arg Met Leu Pro Cys Asp Lys Leu Leu Val Ser Leu Gly Ala 50 55 60

tct cgc ttc tgt ctg cag tca gtg gta atg ggt aag acc att tat gtt 240 Ser Arg Phe Cys Leu Gln Ser Val Val Met Gly Lys Thr Ile Tyr Val 65 70 75 80

ttc ttg cat ccg atg gcc ttc cca tac aac cct gta ctg cag ttt cta 288
Phe Leu His Pro Met Ala Phe Pro Tyr Asn Pro Val Leu Gln Phe Leu
85 90 95

gct ttc cag tgg gac ttc ctg aat gct gcc acc tta tgg tcc tct acc 336 Ala Phe Gln Trp Asp Phe Leu Asn Ala Ala Thr Leu Trp Ser Ser Thr 100 105 110

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115 120 125

gto Val	Phe 130	Phe	tgg Trp	cta Leu	aag Lys	cac His 135	aag Lys	ttg Leu	tct Ser	ggg	tgg Trp 140	Leu	cca Pro	tgg Trp	atg Met	432 .
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cct Pro	tgg Trp	aat Asn	gtc Val 180	act Thr	ggc Gly	gat Asp	agc Ser	ata Ile 185	cgg Arg	agc Ser	tac Tyr	tgt Cys	gag Glu 190	aaa Lys	ttc Phe	576
tat Tyr	ctc Leu	ttc Phe 195	cct Pro	cta Leu	aaa Lys	atg Met	att Ile 200	act Thr	tgg Trp	aca Thr	atg Met	ccc Pro 205	act Thr	gct Ala	gtc Val	624
ttt Phe	ttc Phe 210	att Ile	tgc Cys	atg Met	att Ile	ttg Leu 215	ctc Leu	atc Ile	aca Thr	tct Ser	ctg Leu 220	gga Gly	aga Arg	cac His	agg Arg	672
aag Lys 225	aag Lys	gct Ala	ctc Leu	ctt Leu	aca Thr 230	acc Thr	tca Ser	gga Gly	ttc Phe	cga Arg 235	gag Glu	ccc Pro	agt Ser	gtg Val	cag Gln 240	720
gca Ala	cac His	ata Ile	aag Lys	gct Ala 245	ctg Leu	ctg Leu	gct Ala	ctc Leu	ctc Leu 250	tct Ser	ttt Phe	gcc Ala	atg Met	ctc Leu 255	ttc Phe	768
atc Ile	tca Ser	tat Tyr	ttc Phe 260	ctg Leu	tca Ser	ctg Leu	gtg Val	ttc Phe 265	agt Ser	gct Ala	gca Ala	ggt Gly	att Ile 270	ttt Phe	cca Pro	816
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gct Ala 305	gtg Val	ctg Leu	aag Lys	agt Ser	cgy Arg 310	cgt Arg	tcc Ser	tca Ser	Arg	tgt Cys 315	G1 y 999	aca Thr	cct Pro	tga		957

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<213> Homo sapiens

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Ala Gly Asn Gly Phe Ile Thr Ala Ala Leu Gly Val Glu Trp Val Leu 35 40 45

Arg Arg Met Leu Leu Pro Cys Asp Lys Leu Leu Val Ser Leu Gly Ala 50 55 60

Ser Arg Phe Cys Leu Gln Ser Val Val Met Gly Lys Thr Ile Tyr Val 65 70 75 80

Phe Leu His Pro Met Ala Phe Pro Tyr Asn Pro Val Leu Gln Phe Leu 85 90 95

Ala Phe Gln Trp Asp Phe Leu Asn Ala Ala Thr Leu Trp Ser Ser Thr
100 105 110

Trp Leu Ser Val Phe Tyr Cys Val Lys Ile Ala Thr Phe Thr His Pro 115 120 125

Val Phe Phe Trp Leu Lys His Lys Leu Ser Gly Trp Leu Pro Trp Met 130 135 140

Leu Phe Ser Ser Val Gly Leu Ser Ser Phe Thr Thr Ile Leu Phe Phe 145 150 155 160

Ile Gly Asn His Arg Met Tyr Gln Asn Tyr Leu Arg Asn His Leu Gln 165 170 175

Pro Trp Asn Val Thr Gly Asp Ser Ile Arg Ser Tyr Cys Glu Lys Phe 180 185 190

Tyr Leu Phe Pro Leu Lys Met Ile Thr Trp Thr Met Pro Thr Ala Val 195 200 205

Phe Phe Ile Cys Met Ile Leu Leu Ile Thr Ser Leu Gly Arg His Arg 210 215 220

Lys Lys Ala Leu Leu Thr Thr Ser Gly Phe Arg Glu Pro Ser Val Gln 225 230 235 240

Ala His Ile Lys Ala Leu Leu Ala Leu Leu Ser Phe Ala Met Leu Phe 245 250 255

Ile Ser Tyr Phe Leu Ser Leu Val Phe Ser Ala Ala Gly Ile Phe Pro 260 265 270

Pro Leu Asp Phe Lys Phe Trp Val Trp Glu Ser Val Ile Tyr Leu Cys 275 280 285

Ala Ala Val His Pro Ile Ile Leu Leu Phe Ser Asn Cys Arg Leu Arg 290 295 300

Ala Val Leu Lys Ser Arg Arg Ser Ser Arg Cys Gly Thr Pro 305 310 315

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